

Qy	301	DSTAVALNNEEDPKATEIIIEPSKODKPLIEKLAELIYNNSSPYKETKAEHLQLSGGKKKK	360
Db	301	DSTAVALNNEEDPKATEIIIEPSKODKPLIEKLAELIYNNSSPYKETKAEHLQLSGGKKKK	360
Qy	361	ITVFEKISSTTSFCHOLRWVSRSRSPKNLGNPQASIAOIITVVLGAVIGAIYFGLKND9	420
Db	361	ITVFEKISSTTSFCHOLRWVSRSRSPKNLGNPQASIAOIITVVLGAVIGAIYFGLKND9	420
Qy	421	TGIONAGVLFLLTNQCFSSVSAEELFVEKKPLFHEHISGYRVBSYFGLKLSDLPL	480
Db	421	TGIONAGVLFLLTNQCFSSVSAEELFVEKKPLFHEHISGYRVBSYFGLKLSDLPL	480
Qy	481	MRMLPSIIETCTIYFEMLGKPKADAFPVMMFTLMKNAVSASSMALAIAGOSVSVATLL	540
Db	481	MRMLPSIIETCTIYFEMLGKPKADAFPVMMFTLMKNAVSASSMALAIAGOSVSVATLL	540
Qy	541	MTICFPPMMIIFSGLLVNLTTTIASSWLSWLOPSIPRYGFTALQNHPEFGONPCPLNATGN	600
Db	541	MTICFPPMMIIFSGLLVNLTTTIASSWLSWLOPSIPRYGFTALQNHPEFGONPCPLNATGN	600
Qy	601	NPCNVAATCGEEVLVQGGIDLSPPMGIMKQVHALACMIYFLTIAVYLKLLFLFKKTS	655
Db	601	NPCNVAATCGEEVLVQGGIDLSPPMGIMKQVHALACMIYFLTIAVYLKLLFLFKKTS	655

```

RESULT 2
US-09-245-808-1
; Sequence 1, Application US/09245808
; Patent No. 6513277
; GENERAL INFORMATION:
; APPLICANT: Doyle, L. Austin
; APPLICANT: Abruzzo, Lynne V.
; APPLICANT: Rose, Douglas D.
; TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which
; TITLE OF INVENTION: encodes it
; FILE REFERENCE: ROSS Umb conversion
; CURRENT APPLICATION NUMBER: US/09/245, 808
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/073763
; EARLIER FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 655
; TYPE: PRT
ORGANISM: Human MCF-7/Adrvp cells
US-09-245-808-1

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Query Match	99.4%	Score 3331	DB 4	Length 655
Best Local Similarity	99.4%	Pred. No. 0		
Matches 651	Conservative 1	Mismatches 3	Indels 0	Gaps 0
QY	1	MSSSVVEAFIPVSOQNTNGFPATVSNDDKAFPEGAVLSEPHNICYVKLKSGLPKCRKPYE	60	
Db	1	MSSSVVEAFIPVSOQNTNGFPATVSNDDKAFPEGAVLSEPHNICYVKLKSGLPKCRKPYE	60	
QY	61	KEILSNINGIMKPGNALILGPTGGKSSLLDVLAARKDPSGLSDVLINGABRPANPKCN	120	
Db	61	KEILSNINGIMKPGNALILGPTGGKSSLLDVLAARKDPSGLSDVLINGABRPANPKCN	120	
QY	121	SGYVVDVDMVGTLTVRENLQPSAALRLATTTNTHKEKNERINRVVEELGLDKVADSKVGT	180	
Db	121	SGYVVDVDMVGTLTVRENLQPSAALRLATTTNTHKEKNERINRVVEELGLDKVADSKVGT	180	
QY	181	QPIRSGSGGERKRTISIGMELINDPSLLSDEPTTGLDGSSTANAVALLLGRMSKQGRITIF	240	
Db	181	QPIRSGSGGERKRTISIGMELINDPSLLSDEPTTGLDGSSTANAVALLLGRMSKQGRITIF	240	
QY	241	SIHQPRYSIFKLFDSTLTLLASGRLLMPHGQAQALGFESAGYHCAYNNPADFLDIING	300	
Db	241	SIHQPRYSIFKLFDSTLTLLASGRLLMPHGQAQALGFESAGYHCAYNNPADFLDIING	300	

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QY 301 DSTVALNREDDPATETIIBPSKODKPLIEKLAATLYNNSPVEKKAALHOLSGGKKKK 360
Db 301 DSTVALNREDDPATETIIBPSKODKPLIEKLAATLYNNSPVEKKAALHOLSGGKKKK 360
QY 361 ITVEKEISYTTSPFCHOLRMVSKRSFKNLGNPOASIAOIYTVVGLVGAIFYGLKNDNS 420
Db 361 ITVEKEISYTTSPFCHOLRMVSKRSFKNLGNPOASIAOIYTVVGLVGAIFYGLKNDNS 420
QY 421 TGIQNRAGVLPFLTTNOCFFSSVSAVELFVEVKCLEIHEXISGYRVSSYFLGKLTSLDLP 480
Db 421 TGIQNRAGVLPFLTTNOCFFSSVSAVELFVEVKCLEIHEXISGYRVSSYFLGKLTSLDLP 480
QY 481 MRMLPSIIIFTCTVYMLGLKPKKADAFVMMFLTMVAVASASSMALAIAGQSVSVATLL 540
Db 481 MTMLPSIIIFTCTVYMLGLKPKKADAFVMMFLTMVAVASASSMALAIAGQSVSVATLL 540
QY 541 MTICVPEFMPIPSGLLVNLTIASMLSMLOYSIIPRYGPTALOHNEFLGONFCPLNATGN 600
Db 541 MTICVPEFMPIPSGLLVNLTIASMLSMLOYSIIPRYGPTALOHNEFLGONFCPLNATGN 600
QY 601 NPCNVATCTGEEYLVKQGIIDLSPWGLMKONHVALACMIVIFLTIAVYKLLFLKXY 655
Db 601 NPCNVATCTGEEYLVKQGIIDLSPWGLMKONHVALACMIVIFLTIAVYKLLFLKXY 655

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RESULT 3
US-09-134-001C-5561
; Sequence 5561, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lym Doucetle-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5561
; LENGTH: 270
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5561

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Query Match 57.2% Score 241; DB 4; length 270;
Beet Local Similarity 27.1%; Pred. No. 1,4e-16;
Matches 81; Conservative 55; Mismatches 103; Indels 60; Gaps 12;

Qy 42 ICYRVK-----KSGFLPC-----RKPEKEILSNINGIMKPG-LNALIPTG 83
Db 1 VCLRKRIIMLKXDSRSDYSILEYVRLSKYGVGPKAFOEVLKRNINDVEGERISIMGSG 60
Qy 84 GKSKSLDVLARKOPSGLSGDLVING--APRPAN-----PKCSGYYVODDVMGILT 135
Db 61 SGKTLTLVNLVSIDVMT--KGSITINGQLKELSKNSKQSLDKRKIDIGTIPDYNILNLT 118
Qy 136 VRENIQFSALRLATTMTNHEKNERINRVIEELGLDKVADSKVGFPIRNGSGGRKRTS 195
Db 119 VKENIMTLPLSVQDKDKQIMH--EKYQRIVEKLNISDSD-----KYSELSSGGGRKRTS 170
Qy 196 IGMELITDPSILSDLEPTTGSDSVAANAIVLLLKMSKQ-GRTIIIFSIPORVYSIFKLEF 254
Db 171 AARAPINLPSIIPADEPTGALDSKSTLTLKRLKYNBENFTTILMTWHDVPAFS--N 228
Qy 255 SILLTLASGLRMHNGAQAOLGTFESAGHCEAYNNPAD---PFLDIINGDSRAVALNNE 310
Db 229 RYVIMKKDQIF-----TELYQDDDKQTFYKKIINTQSYLGSINNE 269

```

RESULT 4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 1, 2003, 18:38:41 ; Search time 24.5012 Seconds

(without alignments)
1257.181 Million cell updates/sec

Title: US-09-856-927-2

Perfect score: 3350
Sequence: 1 MSSSNVEFIPVSGNTNGF.....MIVFLTAYLKLPLKXYS 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 127863
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3344	99.8	655	1	ABG2_HUMAN
2	1786.5	53.3	650	1	ABG1_MOUSE
3	835.5	24.9	1049	1	ADP1_YEAST
4	803	24.0	687	1	WHIT_DROME
5	762.5	22.8	679	1	WHIT_CERCA
6	748.5	22.3	677	1	WHIT_LUCIF
7	745	22.2	695	1	WHIT_ANOGA
8	730.5	21.8	709	1	WHIT_ANOAL
9	712.5	21.3	666	1	ABG1_MOUSE
10	704.5	21.0	678	1	ABG1_HUMAN
11	702	21.0	646	1	ABG4_HUMAN
12	690.5	20.6	652	1	ABG5_MOUSE
13	678.5	20.3	652	1	ABG5_MOUSE
14	676.5	20.2	598	1	ABG5_RAT
15	674.5	20.1	651	1	ABG5_HUMAN
16	671	20.0	672	1	ABG8_RAT
17	664	19.8	673	1	ABG8_MOUSE
18	653.5	19.5	1294	1	YOH5_YEAST
19	649.5	19.4	666	1	SCRT_DROME
20	637.5	19.0	673	1	ABG8_HUMAN
21	618.5	18.5	610	1	YOSC_CAEEL
22	605.5	18.1	1501	1	SNQ2_YEAST
23	603	18.0	1530	1	BFR1_SCHPO
24	601.5	18.0	1499	1	CDR2_CANAL
25	596	17.8	1511	1	PDR3_YEAST
26	588	17.6	1564	1	PDR3_YEAST
27	579	17.3	1333	1	YN99_YEAST
28	569	17.0	1529	1	PDR2_YEAST
29	537	16.0	1501	1	CDR3_CANAL
30	530.5	15.8	1501	1	CDR3_CANAL
31	527.5	15.7	1511	1	PDR3_YEAST
32	501	15.0	1450	1	CDR4_CANAL
33	483.5	14.4	1410	1	PDR4_YEAST

34	464	13.9	675	1	BROW_DROME
35	445	13.3	668	1	BROW_DROVI
36	237	7.1	355	1	CYGA_SYNY2
37	236.5	7.1	1704	1	ABG3_HUMAN
38	236	7.0	246	1	NATA_BACSU
39	236	7.0	371	1	MAUK_ECOLI
40	236	7.0	1321	1	AB11_HUMAN
41	235.5	7.0	236	1	LIVF_ARCFU
42	232.5	6.9	607	1	HEPA_ANASP
43	227	6.8	1302	1	MDR4_DROME
44	225.5	6.7	576	1	CYDC_HAEIN
45	224	6.7	347	1	NOD1_RHIGA

ALIGNMENTS

RESULT 1
ABG2_HUMAN STANDARD; PRT; 655 AA.
AC 09UNQ0; Q95344; Q9BY73; Q9NUS0;
DT 16-OCT-2001 Rel. 40. Created)
DT 28-FEB-2003 Rel. 41. Last sequence update)
DE ATP-binding cassette, sub-family G, member 2 (Placenta-specific ATP-binding cassette transporter) (Breast cancer resistance protein).
GN ABG2 OR ABCP OR BCRP OR BCRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Placenta;
RC MEDLINE=99065313; PubMed=9850061;
RA Allikmeets K., Schriml L.M., Hutchinson A., Romano-Spica V., Dean M.;
RT "A human placenta-specific ATP-binding cassette gene (ABCP) on chromosome 4q22 that is involved in multidrug resistance.";
Cancer Res. 58:5337-5339(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast cancer;
RA Doyle L.A., Yang W., Abruzzo L.V., Krogmann T., Gao Y., Rishi A.K.,
RT "A multidrug resistance transporter from human MCF-7 breast cancer cells.";
Proc. Natl. Acad. Sci. U.S.A. 95:15665-15670(1998).
RN [3]
RP ERBATUM.
RA Doyle L.A., Yang W., Abruzzo L.V., Krogmann T., Gao Y., Rishi A.K.,
RT Proc. Natl. Acad. Sci. U.S.A. 96:2569-2569(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Kage M., Teukhara S., Sugiyama T., Asada S., Ishikawa E., Teurto T.,
RT "Breast cancer resistance protein contributes a 140-kDa complex as a homodimer.";
Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 198-655 FROM N.A.
RC TISSUE=Placenta;
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagaetsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Yamamoto J., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Niinomiya K., Iwayanagi T.,
RT "Neo human cDNA sequencing project.";
Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.

RX MEDLINE=21474438; PubMed=11590207;
 RA Schmitz G., Langmann T., Heimel S.;
 RT "Role of ABCG1 and other ABCG family members in lipid metabolism.";
 RL J. Lipid Res. 42:11513-1520(2001).
 CC -1- FUNCTION: XENOBOTIC TRANSPORTER THAT APPEARS TO PLAY A MAJOR ROLE
 CC IN THE MULTIDRUG RESISTANCE PHENOTYPE OF A SPECIFIC MCF-7 BREAST
 CC CANCER CELL LINE. WHEN OVEREXPRESSED, THE TRANSEXPOSED CELLS BECOME
 CC RESISTANT TO MITOXANTHRONE, DAUNORUBICIN AND DOXORUBICIN. DISPLAY
 CC DIMINISHED INTRACELLULAR ACCUMULATION OF DAUNORUBICIN, AND
 CC MANIFEST AN ATP-DEPENDENT INCREASE IN THE EFFLUX OF RHODAMINE 123.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
 CC SUBFAMILY.
 CC
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 CC EMBL, AF103736; AAD09188.1; -
 CC EMBL, AF098951; AAC97367.1; -
 CC EMBL, AB056867; BAB39212.1; -
 CC EMBL, AK002040; BAA92050.1; -
 CC Genew; HGNC:74; ABCG2.
 CC MIM, 603756; -
 CC DR GO: 00105021; C: integral to membrane; TAS.
 CC DR GO: 00055524; F: ATP binding activity; TAS.
 CC DR GO: 0004009; F: ATP-binding cassette (ABC) transporter acti. .; TAS.
 CC DR GO: 0005215; F: transporter activity; TAS.
 CC DR GO: 0008559; F: xenobiotic-transporting ATPase activity; TAS.
 CC DR GO: 0009315; P: drug resistance; TAS.
 CC DR GO: 0006932; P: small molecule transporter; TAS.
 CC DR InterPro: IPR003593; AAA_ATPase.
 CC DR InterPro: IPR004339; ABC_transporter.
 CC DR Pfam: PF00005; ABC_tran; 1.
 CC DR ProDom: PD000006; ABC_transporter; 1.
 CC DR SMART, SMO0382; AAA; 1.
 CC DR PROSITE, PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 CC DR PROSITE, PS00893; ABC_TRANSPORTER_2; 1.
 CC KW ATP-binding; Transmembrane; Transport.
 CC FT DOMAIN 1 395
 CC FT TRANSMEM 396 416
 CC FT DOMAIN 417 428
 CC FT TRANSMEM 429 449
 CC FT DOMAIN 450 477
 CC FT TRANSMEM 478 498
 CC FT DOMAIN 499 506
 CC FT TRANSMEM 507 527
 CC FT DOMAIN 528 535
 CC FT TRANSMEM 536 556
 CC FT DOMAIN 557 630
 CC FT TRANSMEM 631 651
 CC FT DOMAIN 652 655
 CC FT NP BIND 80 87
 CC FT CARBOHYD 418 418
 CC FT CARBOHYD 557 557
 CC FT CARBOHYD 596 596
 CC FT CONFLICT 24 24
 CC FT CONFLICT 166 166
 CC FT CONFLICT 208 208
 CC FT CONFLICT 315 315
 CC FT CONFLICT 482 482
 CC FT CONFLICT 482 482
 CC SEQUENCE 655 AA; 72343 MW; 89A6D511DC5CCE0 CRC64;
 CC
 CC Query Match 99.8%; Score 3344; DB 1; Length 655;
 CC Best Local Similarity 99.8%; Pred. No. 3,3e-221;
 CC Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	1	MSSSNVEVFI	PVSGQNTNGP	PAIVSNDLAF	FEQAVLSPHNI	CYVVKLSGFLP	KRKVE	60
Qy	61	KEILISNINGIMK	GLNAILIGPTGG	KSSLLDYLAAK	DPGSLGVLING	APRANFKCN	120	
Db	61	KEILISNINGIMK	GLNAILIGPTGG	KSSLLDYLAAK	DPGSLGVDL	INGAPRANFKCN	120	
Qy	121	SGVVDODDVM	GLTLTYRENL	QPSAALRLAT	TTMTHNEKNER	INRVIEELGLK	VADSKYCT	180
Db	121	SGVVDODDVM	GLTLTYRENL	QPSAALRLAT	TTMTHNEKNER	INRVIEELGLK	VADSKYCT	180
Qy	181	QPIRGVSGGERK	RTSISGMLITD	PSILSDEPTT	GLDSTANAVL	LLLRKMSKOCRTIIF	240	
Db	181	QPIRGVSGGERK	RTSISGMLITD	PSILSDEPTT	GLDSTANAVL	LLLRKMSKOCRTIIF	240	
Qy	241	SIHQPRYSIFKL	FDLSITLLAS	GRLMFHGPAQ	BALCFESAGYH	CEAYNNPADFLDIING	300	
Db	241	SIHQPRYSIFKL	FDLSITLLAS	GRLMFHGPAQ	BALCFESAGYH	CEAYNNPADFLDIING	300	
Qy	301	DSTAVVALNRED	PKATEIIEIP	SKODPPLIEK	LAELYVNS	SPFKETKALHOLSGEKKKK	360	
Db	301	DSTAVVALNRED	PKATEIIEIP	SKODPPLIEK	LAELYVNS	SPFKETKALHOLSGEKKKK	360	
Qy	361	ITVFKKISYTS	FCCHOLRWVS	KRSFKNLIGN	QASIAOIITVTV	GLVIGAIYFGLKND	420	
Db	361	ITVFKKISYTS	FCCHOLRWVS	KRSFKNLIGN	QASIAOIITVTV	GLVIGAIYFGLKND	420	
Qy	421	TGIQNBAGVL	FLITTNOC	FSVSAVELFV	EKKLIEH	EISGYRVSSYFGLKLSDL	480	
Db	421	TGIQNBAGVL	FLITTNOC	FSVSAVELFV	EKKLIEH	EISGYRVSSYFGLKLSDL	480	
Qy	481	MRMLPSII	FTCIYF	FMGLKPRAD	AFVMMFTLM	WVAYSASSMALAIAGOSVVS	540	
Db	481	MRMLPSII	FTCIYF	FMGLKPRAD	AFVMMFTLM	WVAYSASSMALAIAGOSVVS	540	
Qy	541	MTICPVPMMI	FGSLVYNLT	TIASWLSWLO	YFISIPRYG	TALOHNEFGLGONCPGLNATGN	600	
Db	541	MTICPVPMMI	FGSLVYNLT	TIASWLSWLO	YFISIPRYG	TALOHNEFGLGONCPGLNATGN	600	
Qy	601	NPCNVATTCGE	ERLVKQID	LSPMGLMK	NHVALAM	YIPLTIAVLKLLFLKKYS	655	
Db	601	NPCNVATTCGE	ERLVKQID	LSPMGLMK	NHVALAM	YIPLTIAVLKLLFLKKYS	655	

RESULT 2

ABG3_MOUSE

ID	ABG3_MOUSE	STANDARD:	PRT:	650 AA.
AC	Q99P81;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	ATP-binding cassette, sub-family G, member 3.			
GN	ABCG3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
CC	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=5p10en;			
RC	MEDLINE=21030753; PubMed=11178751;			
RA	Mickley L., Jain P., Miyake K., Schriml L.M., Rao K., Fojo T.,			
RA	Bates S., Dean M.;			
RT	"An ATP-binding cassette gene (ABCG3) closely related to the multidrug			
RT	transporter ABCG2 (MXR/ABCP) has an unusual ATP-binding domain.";			
RL	Mamm. Genome 12:88-88(2001).			
CC	-1 SUBUNIT. May dimerize with another subunit to form a functional			
CC	transporter.			
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	-1 TISSUE SPECIFICITY: Highest levels of expression in thymus and			
CC	spleen. Detected in lung and small intestine.			
CC	-1 SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)			
CC	SUBFAMILY.			

RP REVIEW.
 RX MEDLINE=21474438; PubMed=11590207;
 RA Schmitz G., Langmann T., Helmerl S.;
 RT Role of ABCG1 and other ABCG family members in lipid metabolism.";
 RL J. Lipid Res. 42:1513-1520(2001).
 CC -1- FUNCTION: XENOBOTIC TRANSPORTER THAT APPEARS TO PLAY A MAJOR ROLE
 CC IN THE MULTIDRUG RESISTANCE PHENOTYPE OF A SPECIFIC MCF-7 BREAST
 CC CANCER CELL LINE. WHEN OVEREXPRESSED, THE TRANSECTED CELLS BECOME
 CC RESISTANT TO MITOXANTHONE, DAUNORUBICIN AND DOXORUBICIN, DISPLAY
 CC DIMINISHED INTRACELLULAR ACCUMULATION OF DAUNORUBICIN, AND
 CC MANIFEST AN ATP-DEPENDENT INCREASE IN THE EFFLUX OF RHODAMINE 123.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
 CC SUBFAMILY.
 CC -----
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 DR EMBL; AF103796; AAD09188.1; -;
 DR EMBL; AF098851; AAC97367.1; -;
 DR EMBL; AB056867; BAB39212.1; -;
 DR EMBL; AK002040; BAA92050.1; -;
 DR Genew; HGNC:74; ABCG2.
 DR MIM; 603756; -;
 DR GO; GO:0016021; C: integral to membrane; TAS.
 DR GO; GO:0005524; F: ATP binding activity; TAS.
 DR GO; GO:0004009; F: ATP-binding cassette (ABC) transporter acti. . .; TAS.
 DR GO; GO:0005159; F: xenobiotic-catalytic activity; TAS.
 DR GO; GO:0009315; P: drug resistance; TAS.
 DR GO; GO:0006832; P: small molecule transport; TAS.
 DR InterPro; IPR003439; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SMO0382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KM ATP-binding; Transmembrane; Transport.
 FT DOMAIN 1 395
 FT TRANSMEM 396 416
 FT DOMAIN 417 428
 FT TRANSMEM 429 449
 FT DOMAIN 450 477
 FT TRANSMEM 478 498
 FT DOMAIN 499 506
 FT TRANSMEM 507 527
 FT DOMAIN 528 535
 FT TRANSMEM 536 556
 FT DOMAIN 557 630
 FT TRANSMEM 631 651
 FT DOMAIN 652 655
 FT NP_BIND 80 87
 FT CARBOHYD 418 418
 FT CARBOHYD 557 557
 FT CARBOHYD 596 596
 FT CONFLICT 24 24
 FT CONFLICT 166 166
 FT CONFLICT 208 208
 FT CONFLICT 315 316
 FT CONFLICT 482 482
 SO SEQUENCE 655 AA; 72343 MW; 89A6D3511DC5C6C0 CRC64;
 Query Match 81.0%; Score 623; DB 1; Length 655;
 Best Local Similarity 81.6%; Pred. No. 2; 9e-48;
 Matches 120; Conservative 8; Mismatches 17; Indels 2; Gaps 1;
 1 PGCAEAYTASMAALAIATGQSVSVATLMTIAFVPMMLFSGLVNLTITIGWMLSLQY 60

DB 511 FLTMVAAYASASSMALAIAGQSVSVATLMTICVPMMLFSGLVNLTITIGWMLSLQY 570
 QY 61 PSIPRYGFTALQYNEPLGQPCGRVNDNSTCVNSYATCTGNEFLINDGIELSWGLWK 120
 DB 571 PSIPRYGFTALQYNEPLGQPCGRVNDNSTCVNSYATCTGNEFLINDGIELSWGLWK 628
 QY 121 NHVALACMTIIFLTAYLKLFLPKKYS 147
 DB 629 NHVALACMTIIFLTAYLKLFLPKKYS 655
 RESULT 2
 ABG3_MOUSE STANDARD; PRT; 650 AA.
 ID 09981;
 AC 28-FEB-2003 (Rel. 41; Created)
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE ATP-binding cassette, sub-family G, member 3.
 GN ABCG3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21030753; PubMed=1178751;
 RA Mckieley L., Jain P., Miyake K., Schriml L.M., Rao K., Fojo T.,
 RT Bates S., Dean M.;
 RT "An ATP-binding cassette gene (ABCG3) closely related to the multidrug
 RT transporter ABCG2 (MR/ABCP) has an unusual ATP-binding domain.";
 RL Mamm. Genome 12:86-88(2001).
 CC -1- SUBUNIT: May dimerize with another subunit to form a functional
 CC transporter.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- TISSUE SPECIFICITY: Highest levels of expression in thymus and
 CC spleen. Detected in lung and small intestine.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)
 CC SUBFAMILY.
 CC -1- CAUTION: Seems to have a defective ATP-binding region.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF324242; AAK14241.1; -;
 DR MGI; MGI:1351624; Abcg3.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KM Transmembrane; Transport.
 FT DOMAIN 1 387
 FT TRANSMEM 388 408
 FT DOMAIN 409 420
 FT TRANSMEM 421 441
 FT DOMAIN 442 469
 FT TRANSMEM 470 490
 FT DOMAIN 491 498
 FT TRANSMEM 499 519
 FT DOMAIN 520 527
 FT TRANSMEM 528 548
 FT DOMAIN 549 623
 FT TRANSMEM 624 644
 FT DOMAIN 645 648
 SO SEQUENCE 650 AA; 73623 MW; 86A5ABR4DD26971C CRC64;

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RESULT 1
US-09-245-808-1
; Sequence 1, Application US/09245808
; Patent No. 6313277
; GENERAL INFORMATION:
; APPLICANT: Doyle, L. Austin
; APPLICANT: Abruzzo, Lynne V.
; APPLICANT: Ross, Douglas D.
; TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which
; TITLE OF INVENTION: encodes it
; FILE REFERENCE: Ross Umb conversion
; CURRENT APPLICATION NUMBER: US/09/245,808
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/073763
; EARLIER FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Human MCF-7/AdrVp cells
US-09-245-808-1

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Query Match 81.0%; Score 623; DB 4; Length 655;
Best Local Similarity 81.6%; Pred. No. 1.9e-62;
Matches 120; Conservative 8; Mismatches 17; Indels 2; Gaps 1;

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Qy      1 FGLGARAYTASSMALAIATGQS4VSVSATLLMTIAFVFMMFLSGLLVNLRTIGPWSLWLY 60
Db      511 FTLMWVAYSASSMALAIAAGQSVSVSATLLMTICFVFMMIFSGLLVNLTITIASWSLWLY 570

Qy      61 FSIPRYGFTALQYNEFLGQEFCGFNVTDNSTCVNSYAICTGNEYLINQGIELSPWGLWK 120
Db      571 FSIPRYGFTALQHNEFLGNFCPLGNATGNNPC--NYATCTGEELYVKQIGIDLSPWGLWK 628

Qy     121 NHVALACMIIFLTIIAYLKLLFLKKYS 147
Db     629 NHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 2
US-09-767-594-1
; Sequence 1, Application US/09767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Bates, Susan
; APPLICANT: Robey, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services